IN THE SPECIFICATION:

Please replace the paragraph beginning at page 10, line 25, with the following rewritten paragraph:

Figure 1 is a view showing the relationship among the target nucleotide sequence, GTAGTCAGGCCAT (SEQ ID NO:3), the probe, ATGGCCTGAC (SEQ ID NO:1), ~~and~~ the complementary sequence, GTCAGGCCAT (SEQ ID NO:2) / ATGCGTTAACT (SEQ ID NO: 5) and subsequence, ATGCGCGTAAGT (SEQ ID NO: 4), of the present invention;

Please replace the paragraph beginning at page 11, line 22, with the following rewritten paragraph:

Figure 12 is a view showing processes that are carried out by the pseudo-code shown in Figure 9 to obtain evaluation results for a target nucleotide sequence, CGCGCATGAA (SEQ ID NO: 6), in the present invention;

Please replace the paragraph beginning at page 12, line 23, and continuing to page 13, line 8, with the following rewritten paragraph:

Figure 1 is a view showing the relationship among a target nucleotide sequence T, a probe P, and a complementary sequence Q. As shown in Figure 1(a), in a specific embodiment of the present invention, if the probe P is defined as P = ATGGCCTGAC (SEQ ID NO:1), Q that is a sequence complementary to P is defined as Q = GTCAGGCCAT (SEQ ID NO:2). It should be noted that, as shown in Figure 1(a), the relationship between the probe P and the complementary sequence Q is such that not only each nucleotide of the probe P is substituted by each complementary nucleotide in the complementary sequence Q, but also the complementary sequence Q is opposite in direction to the probe P as shown with an arrow AL. Moreover, it is the process of the evaluation of the present invention that the complementary sequence Q is a sequence portion, which constitutes a portion of the target nucleotide sequence T in the maximum edit distance designated by the user, where T is defined as T=GTAGTCAGGCCAT (SEQ ID NO:3).

Please replace the paragraph beginning at page 14, line 1, with the following rewritten paragraph:

Figure 1(b) is a view showing a step of determining the above described edit distance, using a specific embodiment. The figure shows an embodiment in which the subsequence S = ATGCGCGTAAGT (SEQ ID NO: ~~3~~ 4) and the complementary sequence Q = ATGCGTTAACT (SEQ ID NO: ~~4~~ 5). In the embodiment shown in Figure 1(b), the edit distance between the subsequence S and the complementary sequence Q is 4, and the similarity r = (11-4)/11 = 0.6364. Figure 1(b) shows each of a partial sequence Tq and the complementary sequence Q in a proper alignment (hereinafter, the above-described step is referred to as an alignment). In the embodiment shown in Figure 1(b), since deletion takes place twice and each of substitution and insertion takes place once, the edit distance is 4.

Please replace the paragraph beginning on page 23, line 13, and continuing to page 24, line 4, with the following rewritten paragraph:

Figure 11 is a view showing evaluation result obtained by the screening method of the present invention in the form of a table. In the embodiment shown in Figure 11, the target nucleotide sequence T is CGCGCATGAA (SEQ ID NO: ~~5~~ 6), the complementary sequence Q is GCCCATGC, and the edit distance k is 3. The evaluation result obtained by the screening method of the present invention will be explained below with reference to Figure 11. The vertical column of the table of Figure 11 represents the value of the edit distance counter i, the lateral column represents the value of probe_position indicating a position in the complementary sequence, and each value in the table represents the value of position[i] at the time of termination of the evaluation step in Figure 7. In the embodiment shown in Figure 11, since the maximum edit distance k is 3, calculation is carried out only on those having an edit distance i of 3 or smaller. In the embodiment shown in Figure 11, the calculation of positions[i, probe_position] finally proceeds to ② of the pseudo-code shown in Figure 11, and 7 is obtained as a value of positions[3]. Accordingly, 7 is returned as a returned value, and during this routine, the final value of min_k is 2. With regard to the above described positions[i, probe_position], when positions[i, probe_position] is j, the positions[i] becomes

prob_position[i, j]. This sequence data may be stored as a table, or as explained in the present invention, only the value of position[i] with respect to the variable of probe_position that is under evaluation may be stored.